

<!--StartFragment-->ZCCHV_RAT

ID ZCCHV_RAT Reviewed; 776 AA.

AC Q8K3Y6;

DT 10-MAY-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-2002, sequence version 1.

DT 25-NOV-2008, entry version 34.

DE RecName: Full=Zinc finger CCCH-type antiviral protein 1;

DE Short=Zinc finger antiviral protein;

DE Short=rZAP;

GN Name=Zc3havl; Synonyms=Zap;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.

RX PubMed=12215647; DOI=10.1126/science.1074276;

RA Gao G., Guo X., Goff S.P.;

RT "Inhibition of retroviral RNA production by ZAP, a CCCH-type zinc

RT finger protein.";

RL Science 297:1703-1706(2002).

RN [2]

RP PROTEIN SEQUENCE OF 227-238; 341-349; 359-371 AND 548-562, AND MASS

RP SPECTROMETRY.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RA Lubec G., Kang S.U., Lubec S.;

RL Submitted (SEP-2007) to UniProtKB.

RN [3]

RP FUNCTION.

RX PubMed=14557641; DOI=10.1128/JVI.77.21.11555-11562.2003;

RA Bick M.J., Carroll J.W., Gao G., Goff S.P., Rice C.M., McDonald M.R.;

RT "Expression of the zinc-finger antiviral protein inhibits alphavirus

RT replication.";

RL J. Virol. 77:11555-11562(2003).

RN [4]

RP SUBCELLULAR LOCATION, NUCLEAR LOCALIZATION SIGNAL, AND NUCLEAR EXPORT

RP SIGNAL.

RX PubMed=15358138; DOI=10.1016/j.bbrc.2004.06.174;

RA Liu L., Chen G., Ji X., Gao G.;

RT "ZAP is a CRM1-dependent nucleocytoplasmic shuttling protein.";

RL Biochem. Biophys. Res. Commun. 321:517-523(2004).

RN [5]

RP RNA-BINDING.

RX PubMed=15542630; DOI=10.1128/JVI.78.23.12781-12787.2004;

RA Guo X., Carroll J.-W., McDonald M.R., Goff S.P., Gao G.;

RT "The zinc finger antiviral protein directly binds to specific viral

RT mRNAs through the CCCH zinc finger motifs.";

RL J. Virol. 78:12781-12787(2004).

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RN      [6]
RP      FUNCTION.
RX      PubMed=17182693; DOI=10.1128/JVI.01601-06;
RA      Mueller S., Moeller P., Bick M.J., Wurr S., Becker S., Guenther S.,
RA      Kuemmerer B.M.;
RT      "Inhibition of filovirus replication by the zinc finger antiviral
RT      protein.";
RL      J. Virol. 81:2391-2400(2007).
RN      [7]
RP      FUNCTION, AND INTERACTION WITH EXOSC5.
RX      PubMed=17185417; DOI=10.1073/pnas.0607063104;
RA      Guo X., Ma J., Sun J., Gao G.;
RT      "The zinc-finger antiviral protein recruits the RNA processing exosome
RT      to degrade the target mRNA.";
RL      Proc. Natl. Acad. Sci. U.S.A. 104:151-156(2007).
CC      -!- FUNCTION: Induces an innate immunity to viral infections by
CC      preventing the accumulation of viral RNAs in the cytoplasm. Seems
CC      to recruit the RNA processing exosome to degrade the target RNAs.
CC      Inhibits Moloney murine leukemia virus, alphavirus and filovirus
CC      replication.
CC      -!- SUBUNIT: Interacts with EXOSC5.
CC      -!- SUBCELLULAR LOCATION: Cytoplasm. Nucleus. Note=Localizes in the
CC      cytoplasm at steady state, but shuttles between nucleus and
CC      cytoplasm in a XPO1-dependent manner.
CC      -!- TISSUE SPECIFICITY: Expressed in the kidney and liver.
CC      -!- DOMAIN: The second and fourth zinc fingers are involved in binding
CC      to specific viral RNAs.
CC      -!- SIMILARITY: Contains 4 C3H1-type zinc fingers.
CC      -!- SIMILARITY: Contains 1 WWE domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AF521008; AAM75358.1; -; mRNA.
DR      UniGene; Rn.42053; -.
DR      PhosphoSite; Q8K3Y6; -.
DR      Ensembl; ENSRNOG00000013948; Rattus norvegicus.
DR      RGD; 628694; Zc3hav1.
DR      HOVERGEN; Q8K3Y6; -.
DR      GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-KW.
DR      GO; GO:0005634; C:nucleus; IEA:UniProtKB-KW.
DR      GO; GO:0003723; F:RNA binding; IEA:UniProtKB-KW.
DR      GO; GO:0008270; F:zinc ion binding; IEA:InterPro.
DR      GO; GO:0009615; P:response to virus; IEA:UniProtKB-KW.
DR      InterPro; IPR004170; WWE.
DR      InterPro; IPR000571; Znf_CCCH.
DR      Pfam; PF00642; zf-CCCH; 1.
DR      PROSITE; PS50918; WWE; 1.
DR      PROSITE; PS50103; ZF_C3H1; 2.

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PE 1: Evidence at protein level;
 KW Antiviral defense; Cytoplasm; Direct protein sequencing;
 KW Metal-binding; Nucleus; Phosphoprotein; Repeat; RNA-binding; Zinc;
 KW Zinc-finger.
 FT CHAIN 1 776 Zinc finger CCCH-type antiviral protein
 FT 1.
 FT /FTId=PRO_0000211344.
 FT DOMAIN 671 758 WWE.
 FT ZN_FING 73 86 C3H1-type 1.
 FT ZN_FING 88 110 C3H1-type 2.
 FT ZN_FING 150 172 C3H1-type 3.
 FT ZN_FING 169 193 C3H1-type 4.
 FT REGION 224 254 Binding to EXOSC5.
 FT MOTIF 69 76 Nuclear localization signal.
 FT MOTIF 284 291 Nuclear export signal.
 FT MOTIF 405 406 Nuclear localization signal (Potential).
 FT COMBIAS 343 348 Poly-Ser.
 FT COMBIAS 415 418 Poly-Leu.
 FT COMBIAS 533 536 Poly-Ser.
 FT MOD_RES 270 270 Phosphoserine (By similarity).
 FT MOD_RES 274 274 Phosphoserine (By similarity).
 FT MOD_RES 283 283 Phosphoserine (By similarity).
 FT MOD_RES 325 325 Phosphoserine (By similarity).
 FT MOD_RES 351 351 Phosphoserine (By similarity).
 FT MOD_RES 433 433 Phosphothreonine (By similarity).
 FT MOD_RES 459 459 Phosphoserine (By similarity).
 FT MOD_RES 501 501 Phosphotyrosine (By similarity).
 SQ SEQUENCE 776 AA; 86771 MW; D13F61A9F8E5B552 CRC64;

Query Match 100.0%; Score 4129; DB 1; Length 776;
 Best Local Similarity 100.0%; Pred. No. 1.4e-257;
 Matches 776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADPGVCCFITKILCAHGGRTMLEELLGEIRLPEAQLYELLETAGPDRFVLLLETGGQAGI 60
 |||
 Db 1 MADPGVCCFITKILCAHGGRTMLEELLGEIRLPEAQLYELLETAGPDRFVLLLETGGQAGI 60
 Qy 61 TRSVVATTRARVCRRKYCQRPCDSLHLCKLNLGRCHYAQSQRNLCKYSHDVLSEQNFQI 120
 |||
 Db 61 TRSVVATTRARVCRRKYCQRPCDSLHLCKLNLGRCHYAQSQRNLCKYSHDVLSEQNFQI 120
 Qy 121 LKNHEL SGLNQEELACLLVQSDPFFLPEICKSYKGEGRKQTCGQPQPCERLHICEHFTRG 180
 |||
 Db 121 LKNHEL SGLNQEELACLLVQSDPFFLPEICKSYKGEGRKQTCGQPQPCERLHICEHFTRG 180
 Qy 181 NCSYLNCLRSHNLM DRKVLTIMREHGLSPDVVQNIQD ICNNKHARRNPPGTRAAHPHRRG 240
 |||
 Db 181 NCSYLNCLRSHNLM DRKVLTIMREHGLSPDVVQNIQD ICNNKHARRNPPGTRAAHPHRRG 240

Qy	241	GAHRDRSKSRDRFLHNSLEFLSPVVSPLGSGPPSPDVTCKDLSLEDVSVSDVTQKFYKYLGT	300
Db	241	GAHRDRSKSRDRFLHNSLEFLSPVVSPLGSGPPSPDVTCKDLSLEDVSVSDVTQKFYKYLGT	300
Qy	301	HDRQLSPVSSKAAGVQGSPQMRASQEFSEEDGNLDDIFSRNRSDSSSRASAAKVAQRNE	360
Db	301	HDRQLSPVSSKAAGVQGSPQMRASQEFSEEDGNLDDIFSRNRSDSSSRASAAKVAQRNE	360
Qy	361	AVAMKMGMEVKGKKEAPDIDRVPFLNSYIDGVTMEKASVSGIPGKKFTANDLENLLLLND	420
Db	361	AVAMKMGMEVKGKKEAPDIDRVPFLNSYIDGVTMEKASVSGIPGKKFTANDLENLLLLND	420
Qy	421	TWKNVAKPQDLQTTGRITDSGQDKAFLQNKYGGNPVWASASTHNAPNGSSQIMDETPNVS	480
Db	421	TWKNVAKPQDLQTTGRITDSGQDKAFLQNKYGGNPVWASASTHNAPNGSSQIMDETPNVS	480
Qy	481	KSSTSGFAIKPAIAGGKEAVYSGVQSPRSQVLAVPGEATTPVQSNRLPQSPLSSSSHRAA	540
Db	481	KSSTSGFAIKPAIAGGKEAVYSGVQSPRSQVLAVPGEATTPVQSNRLPQSPLSSSSHRAA	540
Qy	541	ASGSPGKNSTHTSVSPAIESSRMTSDPDEYLLRYILNPLFRMDNHGPKEICQDHLKGCQ	600
Db	541	ASGSPGKNSTHTSVSPAIESSRMTSDPDEYLLRYILNPLFRMDNHGPKEICQDHLKGCQ	600
Qy	601	QSHCDRSHFHLPLYRWQMPVYTTWRDFQDMESIEQAYCDPHVELILIIENHQINFQKMTCD	660
Db	601	QSHCDRSHFHLPLYRWQMPVYTTWRDFQDMESIEQAYCDPHVELILIIENHQINFQKMTCD	660
Qy	661	YPIRRLSTPSYEEKPLSAVFATKWIWYWKNEFNEYIQYGNESPGHTSSDINSAYLESFFQ	720
Db	661	YPIRRLSTPSYEEKPLSAVFATKWIWYWKNEFNEYIQYGNESPGHTSSDINSAYLESFFQ	720
Qy	721	SCPRGVLPPFAGSQKYELSFQGMQIQTNIASKTQRHVVRPVPVSSNDVEQKRRGPE	776
Db	721	SCPRGVLPPFAGSQKYELSFQGMQIQTNIASKTQRHVVRPVPVSSNDVEQKRRGPE	776

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